

Supplemental Table 1. Information on 101 genes analyzed in this study.

| Chromosome | Rice gene | RAP ID | MSU ID ^a | Comparison of rice gene to homologs of the wild relatives ^c | | Known function ^d | Number of mutations in <i>O. sativa</i> ^f | |
|------------|--------------------|--------------|---------------------|--|-----------------------------------|---------------------------------------|--|----------------|
| | | | | 5' region (1 Kb) | Coding region(s) | | 5' region (1 Kb) | Coding regions |
| 1 | <i>ME</i> | Os01g0188400 | Os01g09320.1 | Mixed | Mixed | Malic enzyme | 3 | 5 |
| | <i>CKX2</i> | Os01g0197700 | Os01g10110.1 | New I | New | Cytokinin oxidase | 7 | 5 |
| | <i>ANS1</i> | Os01g0372500 | Os01g27490.1 | On-like ^b | On-like | Flavonoid network | 1 | 5 ^e |
| | <i>DFR</i> | Os01g0633500 | Os01g44260.1 | Mixed | On-like | Flavonoid network | 9 | 4 |
| | <i>NOG1</i> | Os01g0752200 | Os01g54860.1 | New J | Mixed | Grain number | 24 | 2 |
| | <i>CM3</i> | Os01g0764400 | Os01g55870.1 | New I ^b | Mixed | <i>Shikimate pathway</i> | 6 | 2 |
| | <i>iPGAM1</i> | Os01g0817700 | Os01g60190.1 | Mixed ^b | Mixed | <i>Glycolysis</i> | 4 | 0 |
| | <i>qSH1</i> | Os01g0848400 | Os01g62920.1 | <i>O. nivara</i> | Mixed | Seed shattering | 0 | 1 |
| | <i>SD1</i> | Os01g0883800 | Os01g66100.1 | New J | Nearly Identical amino acids (aa) | Gibberellin biosynthesis | 6 | 4 |
| 2 | <i>SBE3</i> | Os02g0528200 | Os02g32660.1 | Or-J & On-I | Or-J & On-I | Starch branching enzyme | 0 | 0 |
| | <i>ZB8</i> | Os02g0627100 | Os02g41680.1 | Mixed | Or-like | Phenylalanine ammonia-lyase | 4 | 1 |
| | <i>TTG1</i> | Os02g0682500 | Os02g45810.2 | Or-J & On-I | Or-J & On-I | WDR gene | 0 | 1 |
| | <i>SK2</i> | Os02g0687500 | Os02g46220.1 | New | Nearly identical aa | <i>Shikimate pathway</i> | 16 | 2 |
| | <i>FLS</i> | Os02g0767300 | Os02g52840.1 | Or-J & On-I | Identical aa | <i>Flavonoid network</i> | 2 | 2 |
| | <i>DTH2</i> | Os02g0724000 | Os02g49230.1 | Or-J & On-I | Or-J & On-I | Flowering | 1 | 1 |
| | | | | | | | | |
| 3 | <i>MADS1</i> | Os03g0215400 | Os03g11614.1 | Mixed | Identical nucleotides (nt) | Grain length | 7 | 0 |
| | <i>CS</i> | not listed | Os03g14990.1 | Mixed | On-like | <i>Shikimate pathway</i> | 4 | 1 |
| | <i>LAR</i> | Os03g0259400 | Os03g15360.2 | Mixed | Mixed | <i>Flavonoid network</i> | 2 | 1 |
| | <i>Unknown</i> | Os03g0330200 | Os03g21260.1 | Mixed | Mixed | Unknown | 6 | 1 |
| | <i>SUS2</i> | Os03g0340500 | Os03g22120.2 | On-like ^b | Identical aa | <i>Sugar metabolism</i> | 3 | 1 |
| | <i>DAHPS1</i> | Os03g0389700 | Os03g27230.1 | New I | New I | <i>Shikimate pathway</i> | 9 | 5 |
| | <i>GS3</i> | Os03g0407400 | not listed | <i>O. rufipogon</i> | <i>O. rufipogon</i> | Grain length | 1 | 1 |
| | <i>MYB3</i> | Os03g0410000 | Os03g29614.1 | Or-like | Or-like | <i>Flavonoid network</i> | 0 | 2 |
| | <i>GL3.2</i> | Os03g0417700 | Os03g30420.1 | New | On-like | Grain development | 22 | 3 |
| | <i>TB1</i> | Os03g0706500 | Os03g49880.1 | Mixed ^b | Or-like | Branching | 2 | 2 |
| | <i>Hd6</i> | Os03g0762000 | Os03g55389.1 | Mixed ^b | Nearly identical aa | Flowering | 2 | 1 |
| | <i>Dst</i> | Os03g0786400 | Os03g57240.1 | Mixed | New J | Regulator of <i>CKX2</i> | 7 | 5 |
| | <i>CHI</i> | Os03g0819600 | Os03g60509.1 | On-like ^b | On-like | Flavonoid network | 2 | 1 |
| | <i>ASA1</i> | Os03g0826500 | Os03g61120.1 | Mixed | Mixed | <i>Amino-acid synthesis</i> | 8 | 1 |
| 4 | <i>An-1</i> | Os04g0350700 | Os04g28280.2 | Or-like | New | Awn development | 5 | 11 |
| | <i>GIF1</i> | Os04g0413500 | Os04g33740.1 | Mixed | Mixed | Grain filling | 10 | 6 |
| | <i>MYB15</i> | Os04g0517100 | Os04g43680.1 | Or-like | Or-like | <i>Stress tolerance</i> | 5 | 3 |
| | <i>An-2</i> | Os04g0518800 | Os04g43840.1 | Mixed | Mixed | Awn length | 4 | 1 |
| | <i>Unknown</i> | Os04g0557200 | Os04g47040.1 | Mixed | New J | Unknown | 2 | 3 |
| | <i>B2</i> | Os04g0557500 | Os04g47059.1 | On-J & Or-I | New J | bHLH gene | 2 | 7 |
| | <i>B1</i> | Os04g0557800 | Os04g47080.1 | Mixed | New | bHLH gene | 1 | 7 |
| | <i>AGO2</i> | Os04g0615700 | Os04g52540.1 | New J | New | Grain length/salt tolerance | 13 | 23 |
| | <i>IPK1</i> | Os04g0661200 | Os04g56580.1 | Mixed | Identical aa | Mineral transport | 2 | 1 |
| | <i>F3H</i> | Os04g0662600 | Os04g56700.1 | Or-J & On-I | New J | Flavonoid network | 6 | 5 |
| | <i>SH4</i> | Os04g0670900 | Os04g57530.1 | Mixed | Or-like | Seed shattering | 7 | 2 |
| | <i>PK3</i> | Os04g0677500 | Os04g58110.1 | Or-J & On-I | Identical aa | <i>Glycolysis</i> | 6 | 4 |
| | <i>SHAT1</i> | Os04g0649100 | Os04g55560.1 | Or-J & On-I | Nearly identical aa | Seed shattering | 2 | 3 |
| | | | | | | | | |
| 5 | <i>Chalk5</i> | Os05g0156900 | Os05g06480.1 | Or-J & On-I | Or-J & On-I | Endosperm chalkiness | 4 | 3 |
| | <i>GS5</i> | Os05g0158500 | Os05g06660.1 | Mixed | New | Grain width | 9 | 8 |
| | <i>qSW5</i> | Os05g0187500 | Os05g09520.1 | Or-like | <i>O. rufipogon</i> | Grain size | 1 | 0 |
| | <i>unknown</i> | Os05g0196600 | Os05g10780.1 | On-J & Or-I | Mixed | Unknown | 7 | 5 |
| | <i>ACC7</i> | Os05g0319200 | Os05g25490.1 | Or-J & On-I | Or-J & On-I | <i>Ethylene synthesis</i> | 1 | 0 |
| | <i>C4H</i> | Os05g0320700 | Os05g25640.1 | Or-J & On-I | Mixed | <i>Cinnamate 4-monooxygenase</i> | 5 | 1 |
| | <i>SH5</i> | Os05g0455200 | Os05g38120.1 | Mixed | Mixed | Seed shattering | 4 | 4 |
| | <i>T6PS</i> | Os05g0518600 | Os05g44210.1 | Mixed | Mixed | <i>Trehalose-6-phosphate synthase</i> | 8 | 6 |
| | | | | | | | | |
| 6 | <i>EPSPS</i> | Os06g0133900 | Os06g04280.1 | New | Identical nt | Shikimate pathway | 4 | 0 |
| | <i>Hd3a</i> | Os06g0157700 | Os06g06320.1 | Mixed | New J | Flowering pathway | 4 | 3 |
| | <i>SSY1</i> | Os06g0160700 | Os06g06560.1 | <i>O. rufipogon</i> ^b | <i>O. rufipogon</i> | <i>Starch metabolism</i> | 0 | 0 |
| | <i>C1</i> | Os06g0205000 | Os06g10340.1 | Or-like | On-like | Flavonoid network | 2 | 1 |
| | <i>TCP19</i> | Os06g0226700 | Os06g12230.1 | Or-like | <i>O. rufipogon</i> | Tillering response to nitrogen | 4 | 0 |
| | <i>Hd1</i> | Os06g0275000 | Os06g16370.1 | Mixed | New I | Flowering pathway | 4 | 6 |
| | <i>3GT</i> | Os06g0291100 | Os06g18790.1 | Mixed | Or-J & On-I | <i>Flavonoid network</i> | 10 | 0 |
| | <i>vATPB1</i> | Os06g0568200 | Os06g37180.1 | Mixed | Mixed | <i>Photosynthesis</i> | 4 | 2 |
| | <i>GL6</i> | Os06g0666100 | Os06g45540.1 | New I | Mixed | Grain length | 5 | 1 |
| 7 | <i>PROG1</i> | Os07g0153600 | Os07g05900.1 | Or-like | Or-like | Growth angle | 3 | 1 |
| | <i>bZIP58</i> | Os07g0182000 | Os07g08420.1 | Or-J & On-I | New | Starch metabolism | 0 | 7 |
| | <i>Rc</i> | Os07g0211500 | Os07g11030.1 | Mixed | Mixed | Flavonoid network | 5 | 4 |
| | <i>SSH1</i> | Os07g0235800 | Os07g13170.1 | New J | New J | Seed shattering | 9 | 4 |
| | <i>Ghd7</i> | Os07g0261200 | Os07g15770.1 | Or-J & On-I | Or-J & On-I | Grain productivity | 4 | 1 |
| | <i>SDR4</i> | Os07g0585700 | Os07g39700.1 | Mixed | Mixed | Seed dormancy | 3 | 10 |
| | <i>BG2</i> | Os07g0603700 | Os07g41240.1 | Mixed | Or-J & On-I | Grain growth | 10 | 1 |
| | <i>DAHPSp</i> | Os07g0622200 | Os07g42960.1 | Mixed | Mixed | <i>Shikimate pathway</i> | 1 | 1 |
| | <i>NADH</i> | Os07g0645400 | Os07g45090.1 | Mixed | Mixed | <i>Energy transportation</i> | 5 | 0 |
| | <i>PRR37</i> | Os07g0695100 | Os07g49460.1 | Mixed | Mixed | Circadian clock | 3 | 3 |
| | | | | | | | | |
| 8 | <i>Hd5(Gdh8)</i> | Os08g0174500 | Os08g07740.1 | Or-J & On-I | Or-J & On-I | Grain productivity | 6 | 2 |
| | <i>SSY3</i> | Os08g0191500 | Os08g07740.1 | On-like | On-like | Starch metabolism | 2 | 7 |
| | <i>APS1</i> | Os08g0345800 | Os08g09230.2 | Or-J & On-I | Or-J & On-I | <i>Starch metabolism</i> | 0 | 0 |
| | <i>CM4</i> | Os08g0441600 | Os08g34290.1 | Mixed | Mixed | <i>Shikimate pathway</i> | 2 | 1 |
| | <i>RAE2</i> | Os08g0485500 | Os08g37890.1 | New | New J | Awnless | 3 | 3 |
| | <i>IPA1</i> | Os08g0509600 | Os08g39890.1 | Or-like | Or-like | Plant architecture | 1 | 0 |
| | <i>SPL16</i> | Os08g0531600 | Os08g41940.1 | Mixed | Mixed | Grain width | 6 | 3 |
| 9 | <i>unknown</i> | Os09g0440600 | Os09g26890.1 | Mixed | Mixed | Unknown | 8 | 5 |
| | <i>unknown</i> | Os09g0440700 | Os09g26900.1 | Mixed | Identical nt | Unknown | 8 | 0 |
| | <i>DEP1</i> | Os09g0441900 | Os09g26999.1 | Mixed | Mixed | Panicle morphology | 4 | 2 |
| | <i>PGI</i> | Os09g0465600 | Os09g29070.1 | Mixed | Mixed | Glycolysis | 4 | 2 |
| | <i>bZIP73</i> | Os09g0474000 | Os09g29820.1 | Or-J & On-I | Or-J & On-I | Cold tolerance | 1 | 0 |
| | <i>PRR95</i> | Os09g0532400 | Os09g36220.1 | Mixed ^b | Mixed | <i>Circadian clock</i> | 1 | 1 |
| | <i>DHQS</i> | Os09g0539100 | Os09g36800.1 | Mixed | Mixed | <i>Shikimate pathway</i> | 6 | 4 |
| 10 | <i>PGMp</i> | Os10g0189100 | Os10g11140.2 | On-like ^b | <i>O. nivara</i> aa | <i>Sugar metabolism</i> | 7 | 3 |
| | <i>F3'H</i> | Os10g0320100 | Os10g17260.1 | Mixed ^b | <i>O. nivara</i> aa | Flavonoid network | 2 | 2 |
| | <i>Ehd1</i> | Os10g0463400 | Os10g32600.1 | Mixed, new I | Or-like | Flowering time | 7 | 1 |
| | <i>DAHPS2</i> | Os10g0564400 | Os10g41480.1 | Or-like | Or-like | <i>Shikimate pathway</i> | 5 | 1 |
| | <i>MYC2</i> | Os10g0575000 | Os10g42430.1 | Mixed | Mixed | <i>Jasmonate signaling</i> | 2 | 1 |
| | <i>NRT1.1B</i> | Os10g0554200 | Os10g40600.1 | Or-like | Mixed | Nitrogen usage | 0 | 1 |
| | | | | | | | | |
| 11 | <i>PK1</i> | Os11g0148500 | Os11g05110.2 | Mixed | Identical aa | <i>Glycolysis</i> | 11 | 0 |
| | <i>unknown</i> | Os11g0181100 | Os11g07910.1 | Mixed | <i>O. nivara</i> aa | Unknown | 8 | 0 |
| | <i>ADH2</i> | Os11g0210500 | Os11g10510.1 | Mixed ^b , new J | <i>O. nivara</i> | <i>Alcohol metabolism</i> | 15 | 0 |
| | <i>unknown</i> | Os11g0483900 | Os11g29350.2 | Mixed | Identical nt | Unknown | 4 | 0 |
| | <i>unknown</i> | Os11g0484500 | Os11g29400.1 | Or-J ^b & On-I ^b | New J | Unknown | 14 | 27 |
| | <i>CHS</i> | Os11g0530600 | Os11g32650.1 | Mixed ^b | Mixed | Flavonoid network | 2 | 3 |
| 12 | <i>unknown</i> | Os12g0108500 | Os12g01760.1 | Or-J & On-I | <i>O. rufipogon</i> | Unknown | 1 | 0 |
| | <i>unknown</i> | Os12g0533700 | Os12g34860.1 | Mixed | Mixed | Unknown | 5 | 3 |
| | <i>SDH2(DHQD2)</i> | Os12g0534000 | Os12g34874.1 | Or-J & On-I | Mixed | <i>Shikimate pathway</i> | 0 | 1 |
| | <i>unknown</i> | Os12g0534700 | Os12g34920.1 | <i>O. rufipogon</i> | <i>O. rufipogon</i> | Unknown | 0 | 0 |
| | <i>unknown</i> | Os12g0578400 | Os12g38920.1 | Or-like | New i | Unknown | 1 | 2 |
| | <i>CM2</i> | Os12g0578200 | Os12g38900.1 | <i>O. rufipogon</i> | <i>O. rufipogon</i> | <i>Shikimate pathway</i> | 0 | 0 |
| | | | | | | | | |
| Subtotal | | | | | | | 478 | 278 |
| Total | | | | | | | 756 | |

^a Gene ID was based on the Nipponbare genome annotated by MSU Rice Genome Annotation Project.

^b Alignable 5' regions were shorter than 1 Kb.

^c The gene types largely followed those of Figure 3, with mixed standing for Type 4.

^d Italic indicates uncharacterized genes, which have protein domains similar to these characterized in other species such as *Arabidopsis thaliana*.

^e Missing sites in *On* lineage.

^f Details see Supplemental Fig. 1.